



RESEARCH ARTICLE

Stability analysis and selection of late blight resistant local potato genotypes using GGE biplot and AMMI analysis

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Abstract

Potato (*Solanum tuberosum* L.) is the fourth most important food crop globally; its production is severely affected by late blight caused by oomycete *Phytophthora infestans* (Mont.) de Bary. The rapid evolution of the pathogen frequently overcomes race-specific resistance genes, necessitating simultaneous identification of stable and resistant genotypes. In the present study, 30 potato genotypes comprising local landraces and released varieties were evaluated across 4 environments (2 locations over 2 consecutive rabi seasons, 2021–22 and 2022–23) using a randomised complete block design (RCBD) with 3 replications. Tuber yield and late blight severity, expressed as relative area under disease progress curve (rAUDPC), exhibited significant genotypic variation and strong genotype $\times$ environment interaction (GEI). Additive main effects and multiplicative interaction (AMMI) and genotype plus genotype-by-environment interaction (GGE) biplot analyses revealed that genotype, environment and their interaction significantly influenced both the traits. Small sized tuber producing local variety Jalpai and improved cultivar Kufri Chipsona 3 combined high and stable tuber yield with consistently low rAUDPC across environments. Chambal Jyoti, Red Bhutan and Tripura Local 3 showed high yield and late blight resistance in specific environments, whereas Kufri Jyoti, although high yielding, was consistently susceptible to late blight. These results identify promising genotypes for direct cultivation in late blight-prone regions and as parents in breeding programmes aimed at combining stable yield with durable resistance.

Keywords: late blight disease; *Phytophthora infestans*; potato; relative area under disease progress curve; stability

Introduction

Potato (*Solanum tuberosum* L.) is a major non cereal food crop contributing significantly to global food and nutritional security. It is widely consumed due to its versatility, high caloric efficiency and richness in vitamins, antioxidants and dietary fibre and this multipurpose usage of potato makes it obvious choice for farmer as well as for consumers globally. Despite its importance, potato production is severely affected by late blight, caused by *Phytophthora infestans* (Mont.) de Bary., which remains one of the most destructive plant diseases worldwide.

This disease, causing widespread crop failure throughout Northern Europe including Ireland, was the main reason for Iris famine (1). Under favourable cool and humid conditions, the disease can cause rapid foliage destruction, leading to drastic yield losses and increased production costs due to intensive fungicide use.

High genetic adaptability of the pathogen to changing environment is one of the main reasons that researchers found it difficult to control (2). Breeding for resistance has historically been relied on major resistance (R) genes introgressed from wild *Solanum* species. Although several R genes, including R1 to R11 identified in wild species *Solanum demissum* Lindl. and also transferred into *S. tuberosum* (3–5) and some broad-spectrum genes such as RB/Rpi-blb1, Rpi-blb2, Rpi-sto1 and R8, have been deployed, the high

genetic variability and adaptive capacity of have frequently rendered these genes ineffective. Thus, identifying genotypes with stable and durable resistance across environments, coupled with acceptable tuber yield, remains a central objective in potato improvement programmes.

Multi-environment trials are very much crucial for evaluating genotype performance, as genotype $\times$ environment interaction (GEI) can significantly influence both yield and disease response (6). Statistical tools such as additive main effects and multiplicative interaction (AMMI) (7) and genotype plus genotype-by-environment interaction (GGE) biplot analyses are widely used to dissect GEI, identify stable and broadly adapted genotypes and detect specific adaptation to particular environments (8). Both methods are based on principal component analysis (PCA) that assess the relationship between environments, genotypes and genotype with environment. Moreover, the graphical view of results is very much helpful to understand the response of test genotypes in different environments (9). The GGE biplot model have some additional features like ranking of genotypes and environment, the “which-won-where” pattern, mean vs stability as well as discriminating power and representativeness ability of test environment.

The present study aimed to identify promising late blight resistant potato cultivars with stable tuber yield over years by using GGE and AMMI biplot approaches across multiple environments.

Materials and Methods

Plant material

In this study, 30 local potato cultivars from the Cis-Himalayan region of West Bengal, along with some released varieties, were collected. This germplasm, maintained at Uttar Banga Krishi Viswavidyalaya (UBKV) by the Central Germplasm Conservation Unit under the Directorate of Research, were evaluated. Among these cultivars, Kufri Jyoti, a popular variety in the region, was used as the check variety. Rest were local varieties collected from Assam, Tripura, Coochbehar, Burdwan areas. The complete set of genotypes with their entry name is given in Table 1.

Experimental location and layout

The experiments were conducted during the rabi seasons of 2021–22 and 2022–23 at 2 locations in Coochbehar district, West Bengal. The trials were laid out in a randomised complete block design (RCBD) with 3 replications at each location. Each environment was defined as a unique combination of location and year, resulting in 4 test environments (E1–E4). The details of location and layout were presented in Table 2. Environments were represented by combination of seasons and location. The details of environment were shown in Table 3.

Statistical analysis

The AMMI model was used to evaluate the stability, yield and progress of disease of 30 potato cultivars in 2 locations over 2 years. The AMMI analysis partitioned the total variation into genotype, environment and GEI effects. Additive variance was separated from multiplicative variance in AMMI model and then PCA was applied to explain interaction pattern in more detail. The AMMI model is based on principal component axes derived from genotype × environment interaction and is typically presented through AMMI biplots. In contrast, GGE biplot analysis uses

genotype and genotype × environment effects and is visualised separately from AMMI. Both AMMI and GGE biplot methods were employed to evaluate genotype performance and to identify possible mega-environments. The GGE biplot was further used to assess test environments based on their discriminative ability and representativeness, thereby facilitating the identification of an ideal testing environment. The analysis was carried out by using The R statistical package (10).

Results and Discussion

Genotype × environment interaction has important impact in crop improvement and it is crucial for plant breeders to identify stable and adaptable high yielding genotypes under different environmental condition (11). In the present study, performance of genotypes varied across locations and years, indicating a strong influence of environmental factors and GEI on both tuber yield and late blight severity.

Additive main effects and multiplicative interaction analysis of variance for tuber yield and area under disease progress curve trait

The result of the analysis of variance of AMMI model showed that yield and area under disease progress curve (AUDPC) value is significantly ($p < 0.001$) affected by genotype, environment and GEI (Table 4 and 5). The first 2 interaction principal component axes (IPCA1 and IPCA2) together explained 89.7 % and 94.4 % of the GEI variation for potato yield and AUDPC, respectively. Significant GEI were also reported in earlier study for potato tuber yield (12).

Additive main effects and multiplicative interaction 1 stability biplot

In the AMMI 1 biplot, the X-coordinate represents the main effects, which are the genotypes and environment means, while

Table 1. List of potato cultivar used in this study with their location of collection and entry number as treatment

Sl. No.	CGCU Entry No.	Population type	Location of collection	Treatment
1	Jalpai	RSRF	Coochbehar, West Bengal	T1
2	Deshi2	RSWF	Coochbehar, West Bengal	T2
3	Tripura local 1	WSWF	Tripura	T3
4	Tripura local 2	RSWF	Tripura	T4
5	Tripura local 3	RSWF	Tripura	T5
6	Kufri Jyoti	WSWF	ICAR-CPRI, Uttarakhand	T6
7	Kufri Ganga	WSWF	ICAR-CPRI, Uttarakhand	T7
8	Kufri Manik	RSWF	ICAR-CPRI, Uttarakhand	T8
9	Double fun	RSRF	Exotic	T9
10	Kufri Himalini	RSWF	ICAR-CPRI, Uttarakhand	T10
11	Kufri Kanchan	RSWF	ICAR-CPRI, Uttarakhand	T11
12	Kufri Sinduri	WSWF	ICAR-CPRI, Uttarakhand	T12
13	Kufri Frysona	WSWF	ICAR-CPRI, Uttarakhand	T13
14	Kufri Keshar	RSWF	ICAR-CPRI, Uttarakhand	T14
15	Kufri Elar	RSWF	ICAR-CPRI, Uttarakhand	T15
16	Cob local red 2	RSWF	Coochbehar, West Bengal	T16
17	Kufri Giridhari	WSWF	ICAR-CPRI, Uttarakhand	T17
18	Kufri Mohan	WSWF	ICAR-CPRI, Uttarakhand	T18
19	Cob local red 1	RSWF	Coochbehar, West Bengal	T19
20	TP5	RSWF	Tripura	T20
21	Kufri Chipsona 3	WSWF	ICAR-CPRI, Uttarakhand	T21
22	Red Bhutan	RSWF	Bhutan	T22
23	Kufri Lima	WSWF	ICAR-CPRI, Uttarakhand	T23
24	Chambal Jyoti	WSWF	Burdwan	T24
25	Assam local red 2	RSWF	Assam	T25
26	White Bhutan	WSWF	Bhutan	T26
27	Kufri Neelkanth	RSWF	ICAR-CPRI, Uttarakhand	T27
28	Holland	RSWF	Coochbehar, West Bengal	T28
29	Deshi1	RSWF	Coochbehar, West Bengal	T29
30	Assam local red 1	RSWF	Assam	T30

RSWF: red skin white flesh; RSRF: red skin red flesh; WSWF: white skin white flesh; CGCU: central germplasm conservation unit.

Table 2. Details of experimental design and layout

Details	Location 1	Location 2
Experimental site	UBKV Instructional Farm Field, Pundibari, Coochbehar	Block Seed Farm, Sitalkuchi, Coochbehar
Co-ordinates	26° 19' 86" N latitude, 89° 23' 53" E longitude	26° 9' 49" N latitude, 89° 11' 12" E longitude
Plot size	Each plot was 3 m x 2 m	
No. of entries	30	
Design of experiment	Randomised complete block design	
Replications	3	

Table 3. Details of environment

Sl. No.	Location	Year	Code
1	UBKV Instructional Farm Field, Pundibari	2021–22	E1
2	Block seed Farm, Sitalkuchi	2021–22	E2
3	UBKV Instructional Farm Field, Pundibari	2022–23	E3
4	Block seed Farm, Sitalkuchi	2022–23	E4

Table 4. Additive main effects and multiplicative interaction (AMMI) analysis of tuber yield for 30 genotypes evaluated across 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	Proportion	Accumulated
ENV	3	3635313.81	1211771	2.663855	0.119108		
REP (ENV)	8	3639150.71	454893.8	3.539622	0.000691		
GEN	29	132255791	4560545	35.48653	2.44E-69		
GEN: ENV	87	71691502.2	824040.3	6.412026	6.43E-30		
PC1	31	35764896.7	1153706	8.98	0	49.9	49.9
PC2	29	28554747.2	984646.5	7.66	0	39.8	89.7
PC3	27	7371858.28	273031.8	2.12	0.0016	10.3	100
Residuals	232	29815433.4	128514.8				
Total	446	312728694	701185.4				

Df: degrees of freedom; ENV: environment; REP (ENV): replication within environment; GEN: genotype; GEN × ENV: genotype × environment interaction; PC1–PC3: principal components of interaction (IPCA1–IPCA3). Proportion (%) indicates the percentage contribution of each interaction principal component to the total genotype × environment interaction, and accumulated (%) represents the cumulative contribution.

Table 5. Additive main effects and multiplicative interaction (AMMI) analysis of area under disease progress curve (AUDPC) values for 30 genotypes evaluated across 4 environments

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	Proportion	Accumulated
ENV	3	3277342	1092447	433.634	3.42584E-09		
REP (ENV)	8	20154.27	2519.284	0.408202	0.91525061		
GEN	29	47550278	1639665	265.6763	5.3178E-161		
GEN: ENV	87	10666045	122598.2	19.86469	1.14886E-71		
PC1	31	8669101	279648.4	45.31	0	81.3	81.3
PC2	29	1399248	48249.92	7.82	0	13.1	94.4
PC3	27	597696.2	22136.9	3.59	0	5.6	100
Residuals	232	1431826	6171.664				
Total	446	73611690	165048.6				

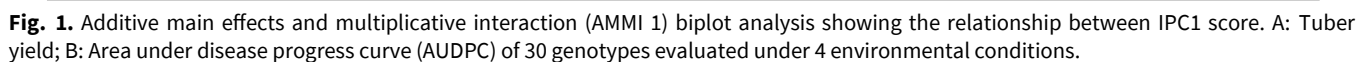
Df: degrees of freedom; ENV: environment; REP (ENV): replication within environment; GEN: genotype; GEN × ENV: genotype × environment interaction; PC1–PC3: principal components of interaction (IPCA1–IPCA3). Proportion (%) indicates the percentage contribution of each principal component to the total genotype × environment interaction and accumulated (%) represents the cumulative contribution.

the interaction effect which is IPCA1 is represented by the Y-coordinate. Both main effects and IPCA1 scores of environments and genotypes were plotted against each other for yield and AUDPC, respectively (Fig. 1A and B). Vertical line in the middle of the graph passes through the average of entire trial. Genotypes and environments on the right side of the graph have yield or AUDPC value higher than the average. Likewise genotypes and environment on the left side of this line have yield or AUDPC value that are lower than the average. The horizontal axis in the middle of the diagram shows the first interaction component that passes through zero point, an area without interaction. Genotypes and location showing higher interaction have larger values for the first principal component of interaction. The genotypes and environment which are closer to the horizontal line show less interaction.

In the yield biplot, improved cultivars like Chambal Jyoti, Kufri lima, Kufri Chipsona 3 and Red Bhutan positioned to the right of the grand mean, were identified as high-yielding, whereas varieties like Tripura Local 1, Tripura local 2 which were positioned to the left side of the grand mean, indicating lower yield. One

environment (E2) was found close to the horizontal line with positive IPCA 1 score expressing less interaction. The E4 was placed distantly from the origin, followed by E3 indicating high interaction with rest of the environment for tuber yield trait. Lastly E1 shows low interaction with other environments.

In the AMMI 1 biplot, genotypes with IPCA1 scores near zero were well adapted in general environment and they were considered stable since they have small interaction effect. In quadrant I, Cultivars like Assam local red 2, Kufri Himalini, Tripura local 3 have positive IPCA 1 scores but below average yield. Quadrant III includes cultivars like Assam local Red 2, Tripura local 1 and Tripura local 2 with negative IPCA scores and below average yield. Several local red skinned types such as Cob local red 1 and Cob local red 2 and small tuber sized producing genotypes like Deshi 1 and Deshi 2 have IPCA 1 values close to zero indicates stability with minimal GEI interaction. However, these stable genotypes are low yielding making them unsuitable for cultivation. Quadrant II comprises genotypes Chambal Jyoti, Kufri Lima, Red Bhutan, Kufri Chipsona 3 were characterised by positive IPCA 1 scores and above average yield. Quadrant IV contains genotypes



score close to zero as well as lower mean AUDPC suggesting that their low AUDPC is expressed consistently across all four environments and therefore represents stable resistance.

The E1 with negative IPCA 1 score is favourable for genotypes like Deshi 1, Deshi 2, Tripura local 1 which also have negative IPCA 1 scores. It indicates that these genotypes express strong resistance to late blight of potato under specific environment conditions like E1. These results are like findings in sugar beet (13), in desi cotton (14), in Bambara groundnut genotypes (15).

The AMMI 2 stability biplot depicts graphical representation based on first and second principal component effect (PCA 1 and PCA 2) and explain genotypic stability and interaction effect among genotypes and environment. It helps in an easy understanding of the interaction pattern and reveals which genotypes perform best in specific conditions. The IPCA 1 scores of genotypes and environment are plotted in X-coordinate (abscissa) and IPCA 2 scores of genotypes and environment are plotted in Y-coordinate (ordinate). In AMMI analysis, IPCA scores primarily reflect the magnitude and pattern of genotype $\times$ environment interaction rather than yield performance itself. Genotypes with IPCA scores close to zero are considered more stable across environments, whereas those with larger IPCA scores show specific adaptation to environments. The AMMI 2 biplot (IPCA1 vs. IPCA2) facilitates the visualisation of interaction patterns and helps identify genotypes with either broad or specific adaptability based on their interaction effects. Genotypes that are in the vicinity of an environment have specific adaptability with that environment whereas those are located near to origin are considered more stable (16).

For yield biplot analysis IPCA 1 and IPCA 2 explain 49.9 % and 39.8 % of the total variation respectively accounting for 89.7 % of the variation. Similarly, for AUDPC biplot analysis IPCA 1 and IPCA 2 explain 81.3 % and 13.1 % of the total variation, respectively

accounting for 94.4 % of the variation (Fig. 2A and B). In the biplot environmental scores are joined to the origin by side lines. The four environments did not form distinct groups on the plot or clusters near origin which indicate varied interaction patterns with the genotypes. In the AMMI 2 biplot, all environments viz E1, E2, E3 and E4 are connected to the origin are indicative of interactive forces. Among these environments, E2 had shorter spoke and shorter angle with X-coordinate indicate less interaction and ideal for identifying genotypes with high mean performance and adaptability. Likewise, E1 and E4 display long arrows indicating strong interaction forces. This is true for both the traits.

For yield biplot, Genotypes Red Bhutan, Holland, Kufri Neelkanth, Chambal Jyoti, Kufri lima were located at the farthest distance and a polygon is formed by connecting these genotypes (Fig. 2B). Biplot is divided into 5 sectors and environments are connected to the origin. Thus, 2 environments, E2 and E3, fell into similar sector and the vertex genotype for this sector is Kufri lima, indicating this genotype produce high yield in those specific environments. Environment E4 fell into a single sector and the vertex genotype for this sector was Holland. The E1 fell into a single sector and the vertex genotype for this sector was Kufri Neelkanth. Genotypes like Kufri Jyoti, Kufri Elar, Kufri Sinduri, some local varieties like Jalpai, Deshi 1 and Deshi 2 and red skinned varieties like Cob local red 2 were close to the centre and considered to have high stability for tuber yield. Due to minimal impact of $G \times E$ interaction, those genotypes exhibit good performance across various environments (Fig. 2B).

For AUDPC biplot, a polygon is formed by connecting genotypes like Kufri Giridhari, Deshi 2, Tripura local 1 Kufri Ganga and Kufri Kanchan which were located at the maximum distance (Fig. 2A). It indicated that Kufri Kanchan and Kufri Giridhari had high interaction effect and expressed specific adaptability in specific environments like E2 and E3, respectively. Popular cultivars like Kufri Neelkanth, Kufri Mohan, Kufri Jyoti and several local cultivars like Jalpai, Tripura local 2 and Assam Local red 1 were close to the centre and classified stable across all environments (Fig. 2A).

Genotype and environment interaction effect were studied

in potato tuber yield and found that potato yield is highly related to environment and GEI factors (17). Similar result was reported in potato (12) and in Bambara groundnut genotypes (15).

Genotype plus genotype-by-environment interaction biplot graphical analysis

Mega-environment analysis: which-won-where pattern

Considering importance of yield and AUDPC trait for late blight resistance, stability analysis was performed on these 2 traits. The polygon view of the “which-won-where” biplot helps to visualise the interaction patterns between genotypes and environments, mega environment differentiation and specific genotype adaptation. The polygon is created by connecting the genotypes that are farthest from the origin, known as vertex genotypes, ensuring that all other genotypes are included within the polygon. Vertex genotypes are located at the edge of the polygon (18).

In this study, partitioning genotype and genotype by environment interaction through GGE biplot analysis showed that PC1 and PC2 explaining 83.04 % (PC1 accounting for 65.85 % and PC2 contributing for 17.19 % variation) of the total GEI variance for tuber yield. For AUDPC trait PC1 and PC2 accounting for 88.17 % and 8.42 %, respectively, explaining 96.59 % of the total GEI variance.

The rays from the origin partitioned the biplot into several sectors. The vertex cultivar at the intersection of the 2 polygon sides was considered the winning genotype. The winner genotype at each sector was best genotype for that environment. The vertex genotypes were more responsive whereas the genotypes placed within the polygon and close to the origin are less affected by the environments (18).

In the present study for yield trait, the genotypes Chambal Jyoti, Tripura local 3, Tripura local 2, Holland and Kufri Giridhari were found at the vertices of the polygon. These genotypes, being more responsive to environmental variation, were considered as specially adapted genotypes. The 5 rays divide the biplot into 5 sectors and the environments fall into two of them (Fig. 3A). These 2 sectors were denoted as mega environment with different winning cultivars. A mega-environment is an environment where a

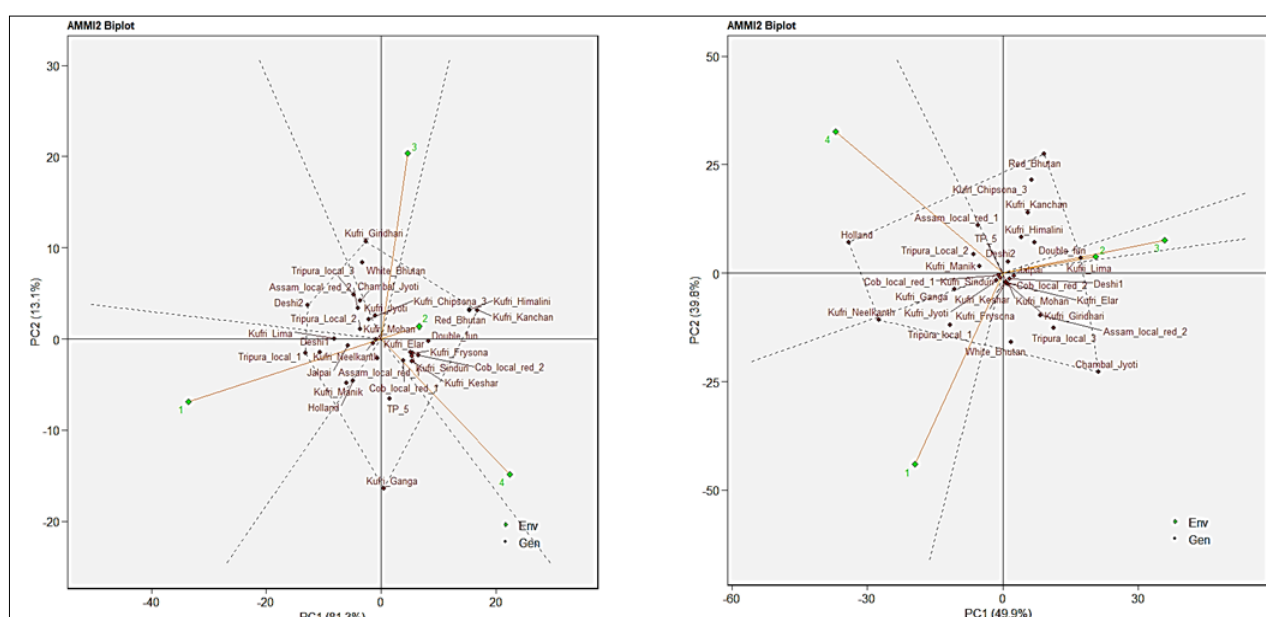


Fig. 2. Additive main effects and multiplicative interaction (AMMI 2) biplot analysis showing the relationship between IPCA1 and IPCA2. A: Area under disease progress curve (AUDPC); B: Tuber yield of 30 genotypes evaluated under four environmental conditions.

specific cultivar or group is adapted particularly. The first mega environment (ME1) was represented by E2 and E3. The vertex cultivar for this sector was Chambal Jyoti, which indicated that this cultivar produces high yield in environmental conditions like E2 and E3. The second mega environment (ME2) was represented by E1 and E4 where Holland was the top performing genotype.

For AUDPC trait, genotypes which were placed at the vertices of polygon were Kufri Jyoti, Kufri Kanchan, Red Bhutan, Assam local red 1, Jalpai, Tripura local 1 and Deshi 2. The 7 rays divide the biplot into 7 sectors and all environments fall into a single sector (Fig. 3B). The mega environment was represented by E1, E2, E3, E4 and Kufri Jyoti was winning genotype in this sector. It indicated Kufri Jyoti was more prone to late blight of potato in all environments.

Like this research, high tuber yielding potato cultivars suitable for wide range of organic environments in Poland were identified by using which-won-where model of GGE biplot (12). High responsive genotype of wheat in heat stressed environment using which-won-where model of GGE biplot were characterised (19, 20). Similar findings were mentioned in various reports (21–23).

Genotype plus genotype-by-environment interaction biplot pattern of “mean vs. stability” analysis for identification of stable genotypes

The mean–stability GGE biplots for tuber yield and AUDPC provide a comprehensive picture of genotype performance and adaptability across the four test environments. These plots partition total variation into a major principal component (PC1), which primarily represents genotype main effects (mean performance) and a second principal component (PC2), which captures the $G \times E$ interaction, i.e., instability. The average environment coordinate (AEC) is depicted as the red axis, constructed from the mean PC1–PC2 scores of all environments and serves as a benchmark against which genotypes are evaluated for both mean response (projection on the AEC) and stability (perpendicular distance from the AEC).

In the yield biplot, the AEC abscissa (red arrow) extends in the direction of increasing mean tuber yield, such that genotypes further along this axis exhibit higher average yield across the test

environments (Fig. 4A). Several improved cultivars, notably Kufri Chipsona 3, Kufri Lima, Chambal Jyoti, Kufri Neelkanth and Holland and small tuber size producing local cultivar like Jalpai occupied positions in the positive direction of PC1, indicating clear superiority in mean yield relative to the overall genotype set. Among these, Kufri Chipsona 3 and Jalpai were located relatively close to the AEC line, suggesting that their high yield is expressed consistently across environments with limited $G \times E$ interaction and they can therefore be regarded as high-yielding and broadly adapted. In contrast, Holland and Kufri Neelkanth exhibited long genotype vectors deviating markedly from the AEC, reflecting high but environment-sensitive yields; these cultivars appear to exploit favourable site-year combinations strongly but show pronounced yield reduction under less suitable conditions.

Several genotypes clustered near the origin of the biplot, including several local, red-skinned types such as Assam local red 1, Assam local red 2, Cob local red 1 and Cob local red 2, together with a subset of older improved varieties. Their proximity to the origin indicated average yield performance combined with moderate interaction, implying neither distinct superiority nor obvious inferiority across environments. These genotypes were agronomically acceptable but, in the presence of clearly superior high-yielding cultivars, offer little advantage for commercial recommendation. Some local types (e.g. Tripura local 1, Tripura local 2 and Tripura local 3) occupy slightly positive positions along the AEC but with noticeable vertical displacement, indicating intermediate yield coupled with specific adaptation to one or two environments rather than broad stability. At the opposite end of the AEC axis, a few genotypes fall in the negative PC1 region; these are consistently low-yielding and, even if comparatively stable, are unsuitable for direct release.

The AUDPC biplot represented the same set of genotypes and environments, but here the trait of interest is cumulative disease progress; hence, lower values along the AEC axis are desirable and correspond to greater resistance. The orientation of the AEC arrow indicated the direction of increasing mean AUDPC, such that genotypes projected in that direction suffer higher disease severity, while those on the opposite side exhibit lower

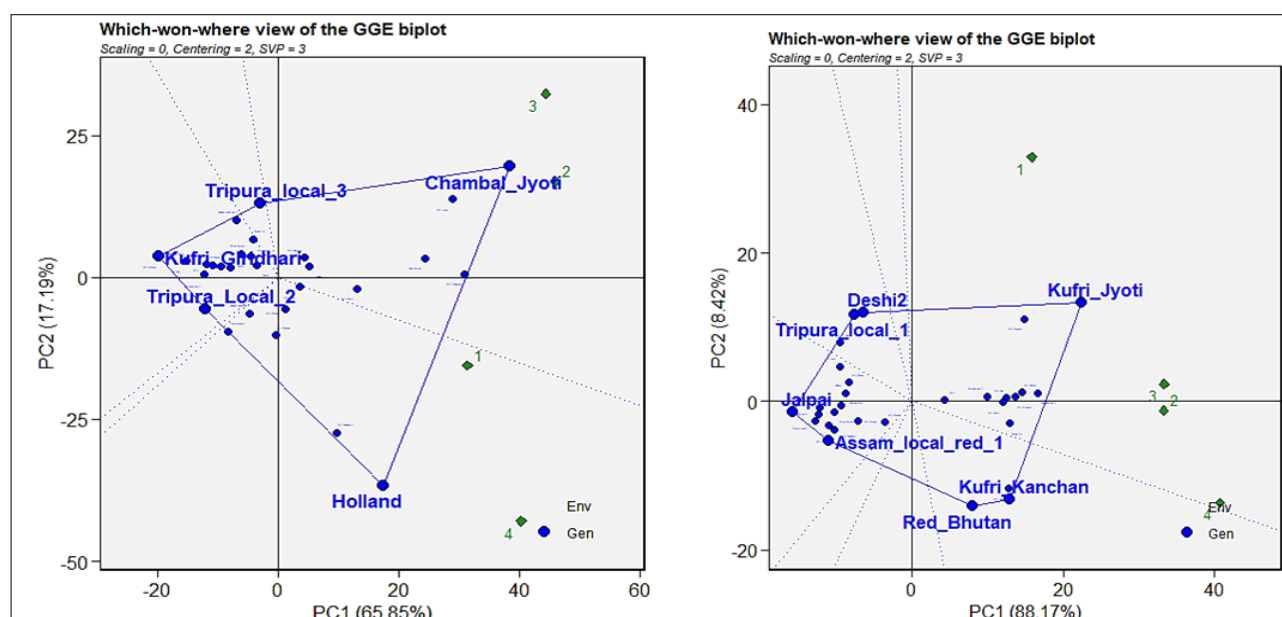


Fig. 3. Genotype plus genotype-by-environment interaction (GGE) biplot (polygon view) showing the which-won-where pattern for potato genotypes. A: Tuber yield; B: Area under disease progress curve (AUDPC).

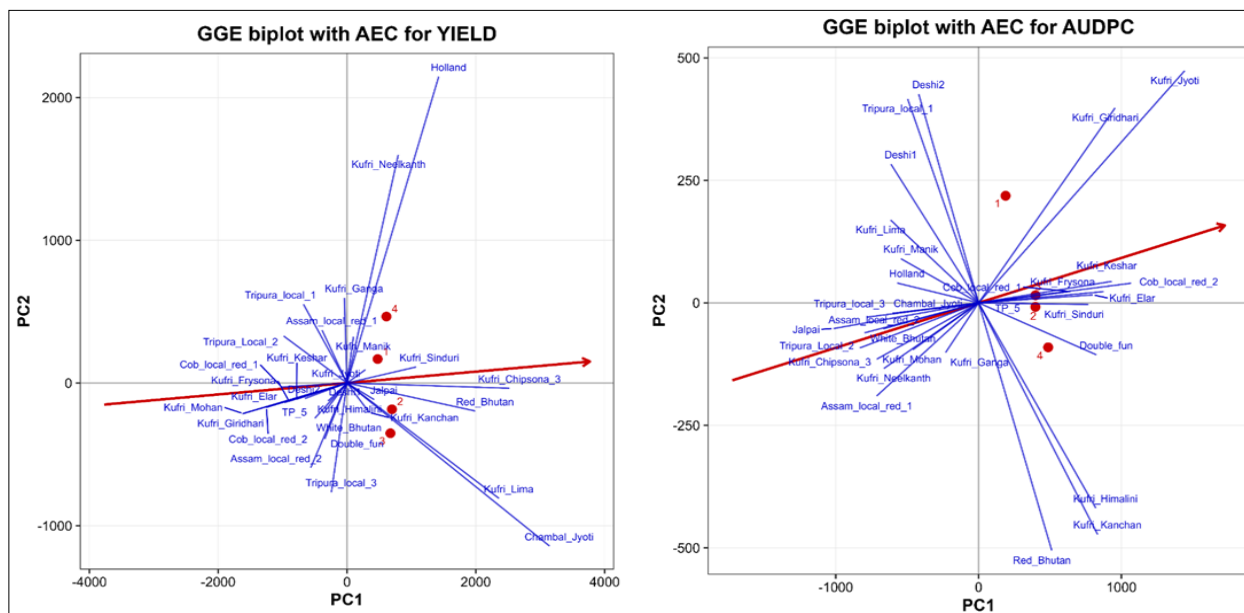


Fig. 4. Genotype plus genotype-by-environment interaction (GGE) biplot showing the mean versus stability pattern. A: Tuber yield; B: Area under disease progress curve (AUDPC).

average AUDPC. In this biplot, some cultivars, including Kufri Jyoti, Kufri Giridhari and a few others, were located close to or in the direction of the AEC arrow and also showed relatively long vectors, indicating not only high mean disease levels but also considerable instability; these genotypes are clearly susceptible and their response is highly environment-dependent (Fig. 4B).

A contrasting group of genotypes lied opposite to the AEC arrow on PC1, indicating lower mean AUDPC and hence better resistance. Varieties like Jalpai, several local, red-skinned types, such as Assam local red 1 and other Assam/Tripura landraces, as well as some improved cultivars, occupied this favorable sector. Many of these genotypes were positioned with relatively short perpendicular distances from the AEC, suggesting that their low AUDPC is expressed consistently across all 4 environments and therefore represents stable resistance rather than site-specific escape. A few genotypes with low mean AUDPC but long vertical displacement from the AEC line can also be noted; these lines show good resistance in some locations but are prone to higher disease pressure in others, reflecting significant $G \times E$ for resistance and indicating specific rather than general adaptability.

The relative placement of environments (red points) also provides insight into the testing network. Environments clustered near the origin behave as average disease pressure sites, whereas those further along PC1 and PC2 are more discriminating and contribute more to the expression of $G \times E$. In the present experiment, one or two environments show pronounced separation along PC1, indicating that they experienced particularly severe or mild epidemics and were therefore critical in differentiating resistant and susceptible genotypes. Such sites could be prioritised for future early-generation screening to maximise selection efficiency for durable resistance.

Discriminateness vs representativeness pattern of genotype plus genotype-by-environment interaction biplot

For the selection of superior genotypes breeder must have to identify best suited test environment. This is a very crucial step for successful breeding programme. An ideal test environment should clearly show the difference between genotypes and at the same time it should be a good representative of target environment. The

test environment without discriminating ability does not provide any kind of information about genotypes is considered as useless. In addition, if a test environment is not representative of target environment is useless as well as misleading.

The “Discriminateness vs representativeness (DVR)” view of GGE biplot assess each test environment based on two criteria (i) the ability of an environment to differentiate between genotypes (discriminateness) (ii) the ability of an environment to reflect other assessed environment (representativeness). Length of the environment vector measures the discriminateness that is longer the length of the environment vector higher is the standard deviation within the environment reflecting high discriminating power. The environment with very short vector is less discriminating and denotes indifference to the performance of the genotypes. The environment at the biplot origin does not provide any information regarding genotypic difference.

In this study for yield and AUDPC trait, Environment E4 exhibited more elongated vector ensuring it has higher discriminating ability among all environment (Fig. 5A and B). It also provided much more information regarding the dissimilarities of genotypes. Henceforth test environment E4 is adjudged as good test environment for identifying widely adapted genotypes. It is followed by E2 and E3.

The assessment of representativeness is measured by the angle between the “average environment axis (AEA)” and the environmental vector. A smaller angle between the investigated environment axis and vector indicates greater representativeness of the mega environment. For yield trait, test environment E2 had minimal angle with AEA and is declared most accurate representative of mega environment and similarly for AUDPC trait test environment E3 having minimal angle with AEA is considered as highly representative. Thus, test environment E2 having small angle with AEA along with long vector indicated that the test environment was greater representative and discriminative.

Similar finding was reported in Bambara groundnut genotypes where assessment of genotype was based on test environments representativeness and discriminating ability (15). Study on mutant rice genotype reported that among the five

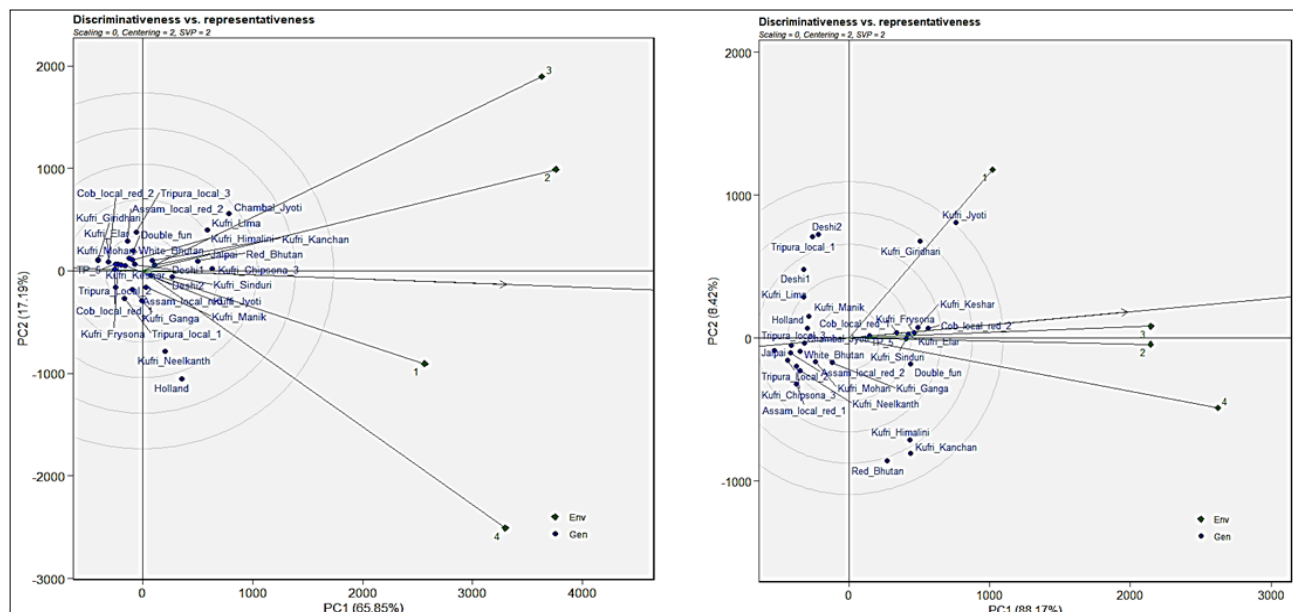


Fig. 5. Genotype plus genotype-by-environment interaction (GGE) biplot showing the discriminativeness versus representativeness pattern. A: tuber yield; B: Area under disease progress curve (AUDPC).

evaluated locations three were noted as ideal location in Malaysia (24).

Genotype ranking for best genotype identification

To rank the genotypes, two coordinate axis are drawn. The first axis is a line joining arrowhead and origin and the line which is perpendicular to it at the origin is second axis. Concentric circles have been created in the biplot. By observing concentric circles along the arrowhead, we can rank the lines based on their inclusion in the circle and their distance from arrowhead on the ordinate.

Therefore, for yield trait, Kufri Chipsona 3 was very close to the ideal line which can be used as reference in genotypic evaluation (Fig. 6B) This genotype was more favourable than all the genotypes in terms of yield and stability. This is followed by Red Bhutan, Kufri Lima and Chambal Jyoti variety. Small tuber producing varieties like Jalpai, Deshi 1 and several improved cultivars like Kufri Sinduri, Kufri Kanchan, Kufri Jyoti genotypes showed stable performance across environments. Kufri Giridhari

and Kufri Mohan had the greatest distance from ideal genotype. This indicated their low stability and low yield across environment.

In case of AUDPC trait, Kufri Jyoti was positioned closer to the centre of the biplot origin indicated high mean AUDPC (Fig. 6A). This reflected the susceptibility of the variety to late blight of potato across the environment. This is followed by genotypes like Cob local red 2, Kufri Giridhari and Kufri Keshar. Jalpai had the greatest distance from ideal genotype. This indicated low AUDPC value across environment. The variety showed resistance against late blight of potato across the environment.

Environment ranking or ideal environment assessment

Ranking of environment is based on ideal environment in which most of the genotypes showed stable performance for various traits studied. Ideal environments have most discriminating and representative feature among other environments. In this study, for tuber yield trait E2 was identified as best location due to being in the closest circle to the centre of the concentric circle followed

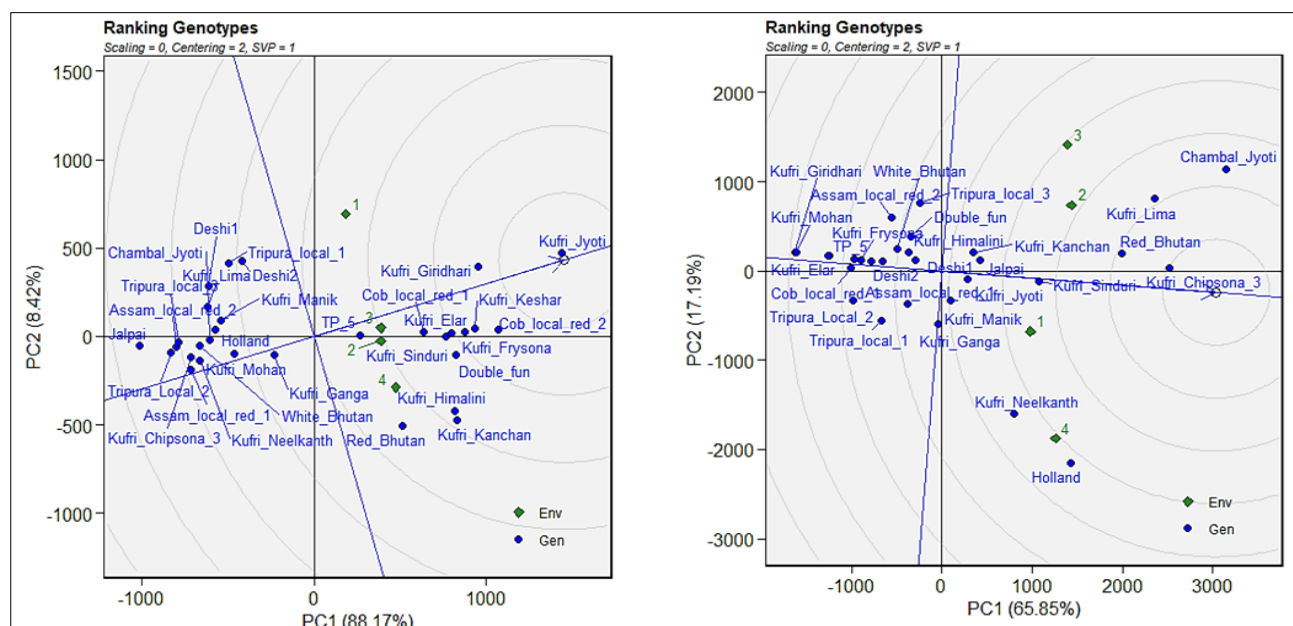


Fig. 6. Genotype plus genotype-by-environment interaction (GGE) biplot showing the genotype ranking pattern. A: Area under disease progress curve; B: tuber yield.

by E1, E3 and E4 (Fig. 7A). E4 was recognised as weakest location due to their greatest distance from the centre of concentric circle. For AUDPC trait E3 followed by E2 and E4 environments were the most favourable environment. Environment E1 was identified as the weakest location (Fig. 7B). Overall, environment E2 was observed to be ideal where maximum genotypes showed stable performance for both traits.

Previous researchers reported ideal environment which is closest to concentric circle similarly identified undesirable environment which was farthest from concentric circle (25). Identification of an ideal environment for assessment of stability of different traits were reported in chrysanthemum hybrid (26) and sugar beet genotypes (13).

Conclusion

The study demonstrated that genotype, environment and their interaction exerted significant effects on potato tuber yield and late blight severity. Multi-environment evaluation through additive main effects and multiplicative interaction and genotype plus genotype-by-environment interaction biplot analyses effectively differentiated genotypes based on yield performance, disease resistance and stability. The local variety Jalpai and the improved cultivar Kufri Chipsona 3 exhibited high yield potential, strong late blight resistance and superior stability, designating them as promising candidates for both direct cultivation and breeding programs. In contrast, high yielding but susceptible cultivars such as Kufri Jyoti and Holland require integration with disease management strategies. Among the test environments, environment 2 (E2) was identified as the most discriminating and reliable for selecting genotypes with wide adaptability and stable resistance to late blight.

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Authors' contributions

PB conducted the experiments, recorded observations, analysed the data and prepared the first draft of the manuscript. SD assisted in data analysis and manuscript preparation. AP and RM contributed to manuscript writing and critically revised the final draft. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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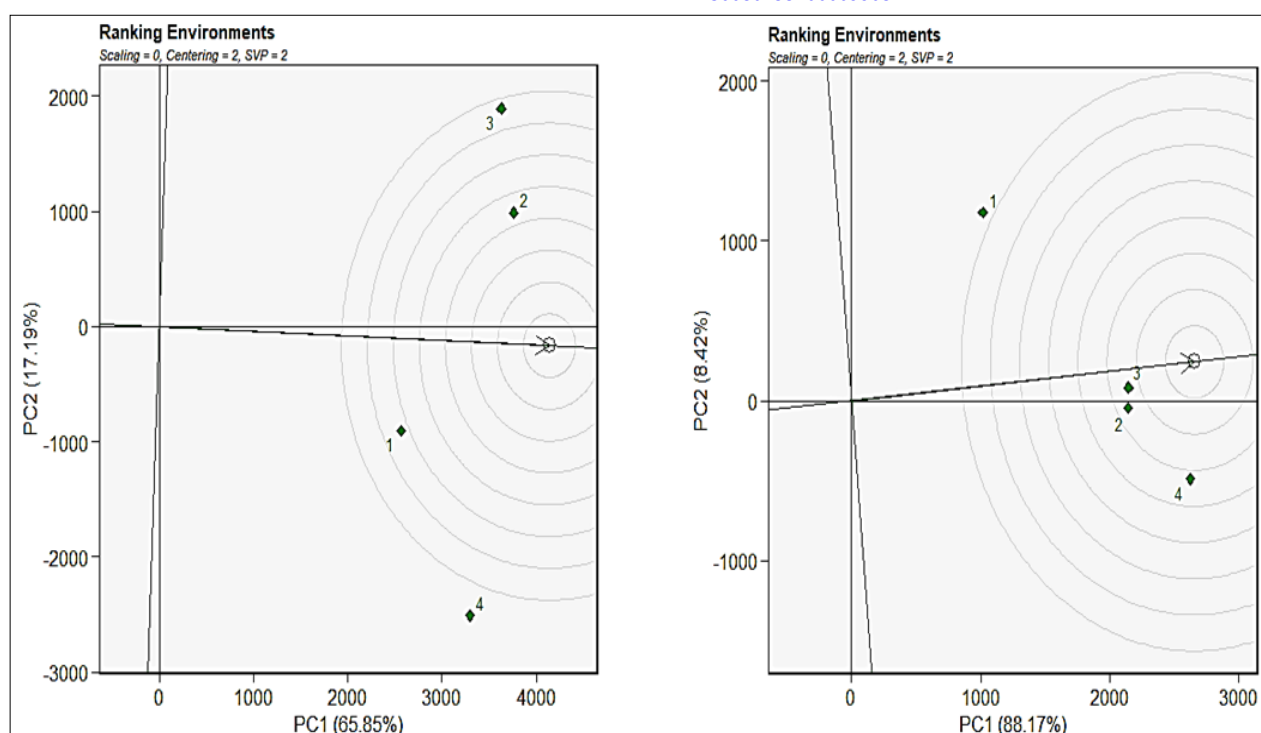


Fig. 7. Genotype plus genotype-by-environment interaction (GGE) biplot showing the environment ranking pattern. A: tuber yield; B: area under disease progress curve (AUDPC).

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